



IFWO

RAW SEQUENCE LISTING

DATE: 07/29/2004

PATENT APPLICATION: US/09/922,181B

TIME: 13:56:51

Input Set : D:\sequence.txt

Output Set : N:\CRF4\07292004\I922181B.raw

1 <110> APPLICANT: Gu, Yizhong
 2 Shannon, Mark
 3 Nguyen, Cung-Tuong
 5 <120> TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7
 AND MDZ12
 7 <130> FILE REFERENCE: AEOMICA-12
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/922,181B
 C--> 9 <141> CURRENT FILING DATE: 2001-08-02
 9 <160> NUMBER OF SEQ ID NOS: 7046
 11 <170> SOFTWARE: Aeomica Sequence Listing Engine
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 1981
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Homo sapiens
 18 <400> SEQUENCE: 1

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 21 ttttgtctga ctctttgcca ccaccctgat ctaagccctt atcatctgct tgaatcacta 180
 22 acttgtctcc acttgacgtt tttaaaagag ttgcttccat ttgacttttt ctgtctgctg 240
 23 taccaacata tgagtttcag gaggggtcat tgatgcagtc attctcagtc tectcggagg 300
 24 gagtctgaag atgcttaaaag agcatccaga gatggcggaa gctcctcagc agcagttggg 360
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 26 tccagagact tttcggctga ggtttcggca gttccgctac caggaggcag ctggacccca 480
 27 ggaagctctt agggggctcc aggagctctg tcgtcgggtg ctgaggcccg agttgcacac 540
 28 caaggagcag atcctggagc tgctggtgct ggagcagttc ctactatcc tgcccccgca 600
 29 gttctacgcc tggatccggg agcatggccc agagagtggc aaggccctgg ccgccatggt 660
 30 ggaggacctg acagaaagag cactggaggc caaggcgggt ccatgccaca ggcagggaga 720
 31 gcaggaggaa acagcacttt gcagaggcgc ttgggagcca ggcattccagc tggggccagt 780
 32 ggagggttaag cctgaatggg ggatgcccc tggggaagga gttcaaggtc cagaccagcag 840
 33 taccgaggag cagctcagtc aggaccctgg agatgagaca cgggccttcc aggagcaagc 900
 34 actacctgtt ctgcaggcgg gtcttgccct ccccgcagtg aatcccagag accaagagat 960
 35 ggcagctggg ttctttactg ctggatcgca ggggttgggg ccatttaaag atatggccct 1020
 36 ggccttccct caggaggagt ggagcatgtg gacccagcc cagatagact gctttgggga 1080
 37 gtatgtggaa gcgcaggact gcagggtctc tccaggcggg gggagcaagg aaaaggaggc 1140
 38 aaaaccccc caggaagacc tgaaaggggc gctggtggca ctgacatcag agaggtttgg 1200
 39 ggaagcctct ctccagggcc ctgggctcgg aagggtctgt gagcaggagc ctggtggccc 1260
 40 tgcaggcagt gcgcctgggc ttctctctcc ccagcacggg gccatcccc tgctgacga 1320
 41 agtcaaaacc cacagctcct tctggaagcc tttccagtgc cctgagtgtg ggaaaggatt 1380
 42 cagtcggagc tccaatctcg tcaggcacca gcgaaccac gaagagaagt cttatggctg 1440
 43 tgtggagtgt gggaagggtt ttaccctgag agagtacctg atgaagcacc agagaacca 1500
 44 cctgggaaag aggcctacg tgtgcagcga gtgctggaaa accttcagcc agagacacca 1560
 45 cctggagggtg caccagcgca gccacactgg ggagaagccc cacaagtgcg gggactgctg 1620
 46 gaagagcttc agccgcaggc agcacctgca ggtgcaccgg aggacgcaca ccggggagaa 1680
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ENTERED

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48 gcgtgcccac actggcgaga agccatatgg gtgccagggtg tgcgggaagc gggttcagcaa 1800
49 aggggagcgg ctggtccgac accagagaat ccatacaggg gagaagccct accactgtcc 1860
50 tgcctgcggg cgaagcttca accagagggtc catcctcaac cggcaccaga agaccagca 1920
51 ccgccaggag ccgctggtgc agtgagcata gcagggtggca ggcagcacca tcattcatct 1980
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54 <210> SEQ ID NO: 2

55 <211> LENGTH: 1635

56 <212> TYPE: DNA

57 <213> ORGANISM: Homo sapiens

59 <400> SEQUENCE: 2

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62 ttctcggtga ggtttcggca gttccgctac caggaggcag ctggacccca ggaagctctt 180
63 agggggctcc aggagctctg tcgtcggtgg ctgaggcccg agttgcacac caaggagcag 240
64 atcctggagc tgctggtgct ggagcagttc ctactatcc tgccccgcga gttctacgcc 300
65 tggatccggg agcatggccc agagagtggc aaggccctgg ccgccatggt ggaggacctg 360
66 acagaaagag cactggaggc caaggcggtt ccattgccca ggcagggaga gcaggaggaa 420
67 acagcacttt gcagaggcgc ttgggagcca ggcattccagc tggggccagt ggaggttaag 480
68 cctgaatggg ggatgcccc ttggggaagga gttcaagggtc cagaccagag taccgaggag 540
69 cagctcagtc aggacctgg agatgagaca cgggccttcc aggagcaagc actacctgtt 600
70 ctgcaggcgg gtccctggcct ccccgagtg aatcccagag accaagagat ggcagctggg 660
71 ttctttactg ctggatcgca ggggttgggg ccatttaaag atatggcctt ggccttccct 720
72 gaggaggagt ggaggcatgt gacccagcc cagatagact gctttgggga gtatgtggaa 780
73 ccgcaggact gcagggtctc tccaggcggt gggagcaagg aaaaggaggc aaaaccccca 840
74 caggaagacc tgaaaggggc gctggtggca ctgacatcag agaggtttgg ggaagcctct 900
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76 gcgcctgggc ttctcctcc ccagcacggt gccatcccc tgctgacga agtcaaaacc 1020
77 cacagctcct tctggaagcc tttccagtg cctgagtggt ggaaaggatt cagtcggagc 1080
78 tccaatctcg tcaggcacca gcgaaccac gaagagaagt cttatggctg tgtggagtgt 1140
79 gggaagggtt ttaccctgag agagtacct atgaagcacc agagaacca cctgggaaag 1200
80 aggccctacg tgtgcagcga gtgctggaaa accttcagcc agagacacca cctggagggtg 1260
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82 agccgcaggc agcacctgca ggtgcaccgg aggacgcaca ccggggagaa gccctacacc 1380
83 tgcgagtgtg gcaagagctt cagcaggaat gccaatctgg cgggtgcaccg gcgtgcccac 1440
84 actggcgaga agccatatgg gtgccagggt tgcgggaagc gggttcagcaa aggggagcgg 1500
85 ctggtccgac accagagaat ccatacaggg gagaagccct accactgtcc tgctgcggg 1560
86 cgaagcttca accagagggt catcctcaac cggcaccaga agaccagca ccgccaggag 1620
87 ccgctggtgc agtga 1635

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89 <210> SEQ ID NO: 3

90 <211> LENGTH: 544

91 <212> TYPE: PRT

92 <213> ORGANISM: Homo sapiens

94 <400> SEQUENCE: 3

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95 Met Leu Lys Glu His Pro Glu Met Ala Glu Ala Pro Gln Gln Gln Leu
96 1 5 10 15
98 Gly Ile Pro Val Val Lys Leu Glu Lys Glu Leu Pro Trp Gly Arg Gly
99 20 25 30
101 Arg Glu Asp Pro Ser Pro Glu Thr Phe Arg Leu Arg Phe Arg Gln Phe
102 35 40 45

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104 Arg Tyr Gln Glu Ala Ala Gly Pro Gln Glu Ala Leu Arg Gly Leu Gln
105      50      55      60
107 Glu Leu Cys Arg Arg Trp Leu Arg Pro Glu Leu His Thr Lys Glu Gln
108 65      70      75      80
110 Ile Leu Glu Leu Leu Val Leu Glu Gln Phe Leu Thr Ile Leu Pro Arg
111      85      90      95
113 Glu Phe Tyr Ala Trp Ile Arg Glu His Gly Pro Glu Ser Gly Lys Ala
114      100      105      110
116 Leu Ala Ala Met Val Glu Asp Leu Thr Glu Arg Ala Leu Glu Ala Lys
117      115      120      125
119 Ala Val Pro Cys His Arg Gln Gly Glu Gln Glu Glu Thr Ala Leu Cys
120      130      135      140
122 Arg Gly Ala Trp Glu Pro Gly Ile Gln Leu Gly Pro Val Glu Val Lys
123 145      150      155      160
125 Pro Glu Trp Gly Met Pro Pro Gly Glu Gly Val Gln Gly Pro Asp Pro
126      165      170      175
128 Gly Thr Glu Glu Gln Leu Ser Gln Asp Pro Gly Asp Glu Thr Arg Ala
129      180      185      190
131 Phe Gln Glu Gln Ala Leu Pro Val Leu Gln Ala Gly Pro Gly Leu Pro
132      195      200      205
134 Ala Val Asn Pro Arg Asp Gln Glu Met Ala Ala Gly Phe Phe Thr Ala
135      210      215      220
137 Gly Ser Gln Gly Leu Gly Pro Phe Lys Asp Met Ala Leu Ala Phe Pro
138 225      230      235      240
140 Glu Glu Glu Trp Arg His Val Thr Pro Ala Gln Ile Asp Cys Phe Gly
141      245      250      255
143 Glu Tyr Val Glu Pro Gln Asp Cys Arg Val Ser Pro Gly Gly Gly Ser
144      260      265      270
146 Lys Glu Lys Glu Ala Lys Pro Pro Gln Glu Asp Leu Lys Gly Ala Leu
147      275      280      285
149 Val Ala Leu Thr Ser Glu Arg Phe Gly Glu Ala Ser Leu Gln Gly Pro
150      290      295      300
152 Gly Leu Gly Arg Val Cys Glu Gln Glu Pro Gly Gly Pro Ala Gly Ser
153 305      310      315      320
155 Ala Pro Gly Leu Pro Pro Pro Gln His Gly Ala Ile Pro Leu Pro Asp
156      325      330      335
158 Glu Val Lys Thr His Ser Ser Phe Trp Lys Pro Phe Gln Cys Pro Glu
159      340      345      350
161 Cys Gly Lys Gly Phe Ser Arg Ser Ser Asn Leu Val Arg His Gln Arg
162      355      360      365
164 Thr His Glu Glu Lys Ser Tyr Gly Cys Val Glu Cys Gly Lys Gly Phe
165      370      375      380
167 Thr Leu Arg Glu Tyr Leu Met Lys His Gln Arg Thr His Leu Gly Lys
168 385      390      395      400
170 Arg Pro Tyr Val Cys Ser Glu Cys Trp Lys Thr Phe Ser Gln Arg His
171      405      410      415
173 His Leu Glu Val His Gln Arg Ser His Thr Gly Glu Lys Pro His Lys
174      420      425      430
176 Cys Gly Asp Cys Trp Lys Ser Phe Ser Arg Arg Gln His Leu Gln Val

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177          435          440          445
179 His Arg Arg Thr His Thr Gly Glu Lys Pro Tyr Thr Cys Glu Cys Gly
180          450          455          460
182 Lys Ser Phe Ser Arg Asn Ala Asn Leu Ala Val His Arg Arg Ala His
183 465          470          475          480
185 Thr Gly Glu Lys Pro Tyr Gly Cys Gln Val Cys Gly Lys Arg Phe Ser
186          485          490          495
188 Lys Gly Glu Arg Leu Val Arg His Gln Arg Ile His Thr Gly Glu Lys
189          500          505          510
191 Pro Tyr His Cys Pro Ala Cys Gly Arg Ser Phe Asn Gln Arg Ser Ile
192          515          520          525
194 Leu Asn Arg His Gln Lys Thr Gln His Arg Gln Glu Pro Leu Val Gln
195          530          535          540
200 <210> SEQ ID NO: 4
201 <211> LENGTH: 1521
202 <212> TYPE: DNA
203 <213> ORGANISM: Homo sapiens
205 <400> SEQUENCE: 4
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208 agcatccaga gatggcggaa gctctcagc agcagttggg tattcctgtg gtgaaactgg 180
209 agaaagagtt gccatggggc agaggaaagg aggaccctag tccagagact ttctggctga 240
210 ggttttcggca gttccgctac caggaggcag ctggacccca ggaagctctt agggggctcc 300
211 aggagctctg tcgtcgggtg ctgaggcccg agttgcacac caaggagcag atcctggagc 360
212 tgctggtgct ggagcagttc ctcactatcc tgccccgcga gttctacgcc tggatccggg 420
213 agcatggccc agagagtggc aaggccctgg ccgccatggt ggaggacctg acagaaagag 480
214 cactggaggc caaggcgggt ccatgccaca ggcagggaga gcaggaggaa acagcacttt 540
215 gcagaggcgc ttgggagcca ggcattccagc tggggccagt ggaggttaag cctgaatggg 600
216 ggatgcccc tggggaagga gttcaaggtc cagaccagg taccgaggag cagctcagtc 660
217 aggaccctgg agatgagaca cgggccttcc aggagcaagc actacctgtt ctgcaggcgg 720
218 gtcctggcct cccgcagtg aatcccagag accaagagat ggcagctggg ttctttactg 780
219 ctggatcgca ggggttgggg ccatttaaag atatggccct ggccttccct gaggaggagt 840
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226 tcaggcacca gcgaaccac gaagagaagt cttatggctg tgtggagtgt gggaaagggt 1260
227 ttaccctgag agagtacctg atgaagcacc agagaaccca cctgggaaag aggcctacg 1320
228 tgtgcagcga gtgctggaaa accttcagcc agagacacca cctggagggtg caccagcgca 1380
229 gccacactgg ggagaagccc cacaagtgcg gggactgctg gaagagcttc agccgcaggc 1440
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233 <210> SEQ ID NO: 5
234 <211> LENGTH: 110
235 <212> TYPE: DNA
236 <213> ORGANISM: Homo sapiens
238 <400> SEQUENCE: 5

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239 tttaaaagag ttgcttccat ttgacttttt ctgtctgctg taccaacata tgagtttcag 60
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242 <210> SEQ ID NO: 6
243 <211> LENGTH: 1411
244 <212> TYPE: DNA
245 <213> ORGANISM: Homo sapiens
247 <400> SEQUENCE: 6
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250 ttccggctga ggtttcggca gtcccgctac caggaggcag ctggacccca ggaagctctt 180
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273 <210> SEQ ID NO: 7
274 <211> LENGTH: 470
275 <212> TYPE: PRT
276 <213> ORGANISM: Homo sapiens
278 <400> SEQUENCE: 7
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282 Gly Ile Pro Val Lys Leu Glu Lys Glu Leu Pro Trp Gly Arg Gly
283 20 25 30
285 Arg Glu Asp Pro Ser Pro Glu Thr Phe Arg Leu Arg Phe Arg Gln Phe
286 35 40 45
288 Arg Tyr Gln Glu Ala Ala Gly Pro Gln Glu Ala Leu Arg Gly Leu Gln
289 50 55 60
291 Glu Leu Cys Arg Arg Trp Leu Arg Pro Glu Leu His Thr Lys Glu Gln
292 65 70 75 80
294 Ile Leu Glu Leu Leu Val Leu Glu Gln Phe Leu Thr Ile Leu Pro Arg
295 85 90 95
297 Glu Phe Tyr Ala Trp Ile Arg Glu His Gly Pro Glu Ser Gly Lys Ala

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date